

# SEQUENCE LISTING

<110> Madden, Mark  
Weiner, David P.  
Chaplin, Jennifer A.

<120> METHODS FOR PRODUCING ENANTIOMERICALLY PURE  
ALPHA-SUBSTITUTED CARBOXYLIC ACIDS

<130> DIVER1440-2

<140> Not yet known

<141> 2000-12-28

<150> 60/254,414

<151> 2000-12-07

<150> 60/173,609

<151> 1999-12-29

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

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<212> DNA

<213> Unknown Organism

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<223> Description of Unknown Organism: Obtained from an  
environmental sample

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<221> CDS

<222> (1)..(1041)

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ccg gtg ttc ctc gat ctc gac gcc aca gtc gag aaa gcg atc gcc ctg 96  
Pro Val Phe Leu Asp Leu Asp Arg Thr Val Glu Lys Ala Ile Gly Leu  
20 25 30

atc gag cag gcg gcc aag cag gac gtg cgc ctg atc gca ttc cca gag 144  
Ile Glu Gln Ala Ala Lys Gln Asp Val Arg Leu Ile Ala Phe Pro Glu  
35 40 45

act tgg att ccc gcc tat ccc ttt tgg ata tgg ctg gcc gcg ccg gct 192  
Thr Trp Ile Pro Gly Tyr Pro Phe Trp Ile Trp Leu Gly Ala Pro Ala  
50 55 60

tgg gcc atg cgc ttc gtc cag cgc tat ttc gag aat tgc ctc gtg cgc 240  
Trp Gly Met Arg Phe Val Gln Arg Tyr Phe Glu Asn Ser Leu Val Arg  
65 70 75 80

ggc agc aag cag tgg cag gcc ctg gcg gat gcg gcc cgc cgc cac gcc 288  
Gly Ser Lys Gln Trp Gln Ala Leu Ala Asp Ala Ala Arg Arg His Gly  
85 90 95

atg cat gtc gcg gcc gcc tat agc gag cgc gcg gcc gcc agc ctc tat 336  
Met His Val Val Ala Gly Tyr Ser Glu Arg Ala Gly Gly Ser Leu Tyr  
100 105 110

sub 7A

09751299 122800

atg ggc cag gcg atc ttc ggc ccc gat ggc gat ctg atc gcc gcg cgc	384
Met Gly Gln Ala Ile Phe Gly Pro Asp Gly Asp Leu Ile Ala Ala Arg	
115 120 125	
cgc aag ctc aag cct acc cat gcg gag cgc acc gtg ttc gcc gag gga	432
Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly Glu Gly	
130 135 140	
gac ggc agc cat ctc gcg gtg cac gat acc gcc atc ggg cgc ctc ggc	480
Asp Gly Ser His Leu Ala Val His Asp Thr Ala Ile Gly Arg Leu Gly	
145 150 155 160	
gcg ctc tgt tgc tgg gag cac atc cag cca ttg tcg aaa tac gcc atg	528
Ala Leu Cys Cys Trp Glu His Ile Gln Pro Leu Ser Lys Tyr Ala Met	
165 170 175	
tac gcc gcc gac gaa cag gtc cac gtc gcg tcg tgg ccg agc ttc agc	576
Tyr Ala Ala Asp Glu Gln Val His Val Ala Ser Trp Pro Ser Phe Ser	
180 185 190	
ctc tat cgc ggc atg gcc tat gcg ctc gga ccg gag gtc aat acc gcc	624
Leu Tyr Arg Gly Met Ala Tyr Ala Leu Gly Pro Glu Val Asn Thr Ala	
195 200 205	
gca agc cag atc tac gcg gtc gag ggc ggc tgc tac gtg ctg gcg tcg	672
Ala Ser Gln Ile Tyr Ala Val Glu Gly Gly Cys Tyr Val Leu Ala Ser	
210 215 220	
tgc gcg acc gtt tcg ccg gag atg atc aag gta ttg gtg gat acg ccc	720
Cys Ala Thr Val Ser Pro Glu Met Ile Lys Val Leu Val Asp Thr Pro	
225 230 235 240	
gac aag gag atg ttc ctc aag gcc ggc ggc ggt ttt gcc atg att ttc	768
Asp Lys Glu Met Phe Leu Lys Ala Gly Gly Gly Phe Ala Met Ile Phe	
245 250 255	
ggg ccc gac ggc cgc gcc ctg gcc gag ccg ctc ccg gag acc gaa gag	816
Gly Pro Asp Gly Arg Ala Leu Ala Glu Pro Leu Pro Glu Thr Glu Glu	
260 265 270	
gga ctg ctg gtc gcc gat atc gac ctc ggc atg atc gcg ttg gcc aag	864
Gly Leu Leu Val Ala Asp Ile Asp Leu Gly Met Ile Ala Leu Ala Lys	
275 280 285	
gcg gcg gcc gat ccg gcg ggc cac tat tca ccg ccc gac gta acg cgg	912
Ala Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr Arg	
290 295 300	
ctg ctg ctg gat cga cgt ccg gcc caa cgc gtc gtc acg ctt gat gcc	960
Leu Leu Leu Asp Arg Arg Pro Ala Gln Arg Val Val Thr Leu Asp Ala	
305 310 315 320	
gca ttc gaa ccg caa aac gag gac aag ggc gac gcg ccc gcg ctg cgc	1008
Ala Phe Glu Pro Gln Asn Glu Asp Lys Gly Asp Ala Pro Ala Leu Arg	
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Val Val Ala Glu Ser Ala Ala Ala Ala Gln	
340 345	

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00822T"122800

<213> Unknown Organism

<223> Description of Unknown Organism: Obtained from an environmental sample

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35 40 45  
Thr Trp Ile Pro Gly Tyr Pro Phe Trp Ile Trp Leu Gly Ala Pro Ala  
50 55 60  
Trp Gly Met Arg Phe Val Gln Arg Tyr Phe Glu Asn Ser Leu Val Arg  
65 70 75 80  
Gly Ser Lys Gln Trp Gln Ala Leu Ala Asp Ala Ala Arg Arg His Gly  
85 90 95  
Met His Val Val Ala Gly Tyr Ser Glu Arg Ala Gly Gly Ser Leu Tyr  
100 105 110  
Met Gly Gln Ala Ile Phe Gly Pro Asp Gly Asp Leu Ile Ala Ala Arg  
115 120 125  
Arg Lys Leu Lys Pro Thr His Ala Glu Arg Thr Val Phe Gly Glu Gly  
130 135 140  
Asp Gly Ser His Leu Ala Val His Asp Thr Ala Ile Gly Arg Leu Gly  
145 150 155 160  
Ala Leu Cys Cys Trp Glu His Ile Gln Pro Leu Ser Lys Tyr Ala Met  
165 170 175  
Tyr Ala Ala Asp Glu Gln Val His Val Ala Ser Trp Pro Ser Phe Ser  
180 185 190  
Leu Tyr Arg Gly Met Ala Tyr Ala Leu Gly Pro Glu Val Asn Thr Ala  
195 200 205  
Ala Ser Gln Ile Tyr Ala Val Glu Gly Gly Cys Tyr Val Leu Ala Ser  
210 215 220  
Cys Ala Thr Val Ser Pro Glu Met Ile Lys Val Leu Val Asp Thr Pro  
225 230 235 240  
Asp Lys Glu Met Phe Leu Lys Ala Gly Gly Gly Phe Ala Met Ile Phe  
245 250 255  
Gly Pro Asp Gly Arg Ala Leu Ala Glu Pro Leu Pro Glu Thr Glu Glu  
260 265 270  
Gly Leu Leu Val Ala Asp Ile Asp Leu Gly Met Ile Ala Leu Ala Lys  
275 280 285  
Ala Ala Ala Asp Pro Ala Gly His Tyr Ser Arg Pro Asp Val Thr Arg  
290 295 300  
Leu Leu Leu Asp Arg Arg Pro Ala Gln Arg Val Val Thr Leu Asp Ala  
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<212> DNA

<213> Unknown Organism

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<223> Description of Unknown Organism: Obtained from an environmental sample

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<221> CDS

<222> (1) .. (1014)

09751299 122800

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Met	Lys	Glu	Ala	Ile	Lys	Val	Ala	Cys	Val	Gln	Ala	Ala	Pro	Ile	Tyr		
1				5					10					15			
atg	gat	ttg	gag	gcg	acg	gtg	gac	aaa	acc	att	gag	ttg	atg	gaa	gaa		96
Met	Asp	Leu	Glu	Ala	Thr	Val	Asp	Lys	Thr	Ile	Glu	Leu	Met	Glu	Glu		
			20					25					30				
gca	gca	cgt	aat	aat	gct	cgt	ctg	atc	gcc	ttt	ccg	gaa	act	tgg	att		144
Ala	Ala	Arg	Asn	Asn	Ala	Arg	Leu	Ile	Ala	Phe	Pro	Glu	Thr	Trp	Ile		
		35					40					45					
cca	ggc	tac	cca	tgg	ttt	ctt	tgg	ctt	gac	tca	cca	gca	tgg	gca	atg		192
Pro	Gly	Tyr	Pro	Trp	Phe	Leu	Trp	Leu	Asp	Ser	Pro	Ala	Trp	Ala	Met		
	50					55					60						
caa	ttt	gta	cgc	caa	tac	cat	gag	aac	tca	ttg	gag	ttg	gat	ggc	cct		240
Gln	Phe	Val	Arg	Gln	Tyr	His	Glu	Asn	Ser	Leu	Glu	Leu	Asp	Gly	Pro		
65					70					75					80		
caa	gct	aag	cgc	att	tca	gat	gca	gcc	aag	cgg	ttg	gga	atc	atg	gtc		288
Gln	Ala	Lys	Arg	Ile	Ser	Asp	Ala	Ala	Lys	Arg	Leu	Gly	Ile	Met	Val		
				85					90					95			
acc	ctg	ggg	atg	agt	gaa	cgg	gtc	ggg	ggc	acc	ctt	tac	atc	agt	cag		336
Thr	Leu	Gly	Met	Ser	Glu	Arg	Val	Gly	Gly	Thr	Leu	Tyr	Ile	Ser	Gln		
			100					105					110				
tgg	ttc	ata	ggc	gat	aat	ggg	gac	acc	att	ggg	gcc	cgg	cga	aag	ttg		384
Trp	Phe	Ile	Gly	Asp	Asn	Gly	Asp	Thr	Ile	Gly	Ala	Arg	Arg	Lys	Leu		
		115					120					125					
aaa	cct	act	ttt	gtt	gaa	cgt	act	ttg	ttc	ggc	gaa	ggg	gat	ggg	tca		432
Lys	Pro	Thr	Phe	Val	Glu	Arg	Thr	Leu	Phe	Gly	Glu	Gly	Asp	Gly	Ser		
	130					135					140						
tcg	cta	gcg	gtt	ttc	gag	acg	tct	gtt	gga	agg	ctg	ggg	ggc	tta	tgc		480
Ser	Leu	Ala	Val	Phe	Glu	Thr	Ser	Val	Gly	Arg	Leu	Gly	Gly	Leu	Cys		
145					150					155					160		
tgt	tgg	gag	cac	ctt	caa	ccg	cta	aca	aaa	tac	gct	ttg	tat	gca	caa		528
Cys	Trp	Glu	His	Leu	Gln	Pro	Leu	Thr	Lys	Tyr	Ala	Leu	Tyr	Ala	Gln		
				165					170					175			
aat	gaa	gag	att	cat	tgt	gcg	gct	tgg	ccg	agc	ttt	agc	ctt	tat	cct		576
Asn	Glu	Glu	Ile	His	Cys	Ala	Ala	Trp	Pro	Ser	Phe	Ser	Leu	Tyr	Pro		
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09/16/2003 11:00:00

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<223> Description of Unknown Organism: Obtained from an
environmental sample
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			20					25					30		
Ala	Ala	Arg	Asn	Asn	Ala	Arg	Leu	Ile	Ala	Phe	Pro	Glu	Thr	Trp	Ile
		35					40					45			
Pro	Gly	Tyr	Pro	Trp	Phe	Leu	Trp	Leu	Asp	Ser	Pro	Ala	Trp	Ala	Met
	50					55					60				
Gln	Phe	Val	Arg	Gln	Tyr	His	Glu	Asn	Ser	Leu	Glu	Leu	Asp	Gly	Pro
65					70					75					80
Gln	Ala	Lys	Arg	Ile	Ser	Asp	Ala	Ala	Lys	Arg	Leu	Gly	Ile	Met	Val
				85					90					95	
Thr	Leu	Gly	Met	Ser	Glu	Arg	Val	Gly	Gly	Thr	Leu	Tyr	Ile	Ser	Gln
			100					105					110		
Trp	Phe	Ile	Gly	Asp	Asn	Gly	Asp	Thr	Ile	Gly	Ala	Arg	Arg	Lys	Leu
		115					120					125			
Lys	Pro	Thr	Phe	Val	Glu	Arg	Thr	Leu	Phe	Gly	Glu	Gly	Asp	Gly	Ser
	130					135					140				
Ser	Leu	Ala	Val	Phe	Glu	Thr	Ser	Val	Gly	Arg	Leu	Gly	Gly	Leu	Cys
145					150					155					160
Cys	Trp	Glu	His	Leu	Gln	Pro	Leu	Thr	Lys	Tyr	Ala	Leu	Tyr	Ala	Gln
				165					170					175	
Asn	Glu	Glu	Ile	His	Cys	Ala	Ala	Trp	Pro	Ser	Phe	Ser	Leu	Tyr	Pro
			180					185					190		
Asn	Ala	Ala	Lys	Ala	Leu	Gly	Pro	Asp	Val	Asn	Val	Ala	Ala	Ser	Arg
		195					200					205			
Ile	Tyr	Ala	Val	Glu	Gly	Gln	Cys	Phe	Val	Leu	Ala	Ser	Cys	Ala	Leu
	210					215					220				
Val	Ser	Gln	Ser	Met	Ile	Asp	Met	Leu	Cys	Thr	Asp	Asp	Glu	Lys	His
225					230					235				240	
Ala	Leu	Leu	Leu	Ala	Gly	Gly	Gly	His	Ser	Arg	Ile	Ile	Gly	Pro	Asp
				245					250					255	
Gly	Gly	Asp	Leu	Val	Ala	Pro	Leu	Ala	Glu	Asn	Glu	Glu	Gly	Ile	Leu

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